Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application.

Listing of Claims:

1. (Currently amended) A method for the detection of cytosine ~~methylations~~ methylation in DNA ~~is hereby characterized in that~~ comprising the steps of:

a) bringing the DNA to be investigated ~~is brought~~ into contact with a cytidine deaminase, whereby the cytidine deaminase deaminates cytidine and 5-methylcytidine at different rates,

b) investigating the partially deaminated DNA ~~is investigated~~ with respect to its sequence, and

c) concluding, from the presence or the proportion of deaminated positions, ~~conclusions can be made on~~ the methylation status of the DNA to be investigated in said positions.

2. (Currently amended) The method according to claim 1, ~~further characterized in that *activation-induced cytidine deaminase – AID* or a biologically active fragment of AID or a modification thereof can be used as the methylation-specific~~ wherein the enzyme AID (activation-induced cytidine deaminase) is used as the cytidine deaminase.

3. (Currently amended) The method according to claim 1, ~~further characterized in that~~ wherein the DNA to be investigated is present at least partially in single-stranded form.

4. (Currently amended) The method according to claim 1, further ~~characterized in that~~

comprising hybridizing the DNA to be investigated ~~hybridizes~~ with oligomers, whereby the hybrids are present in single-stranded form at the cytosine positions under investigation.

5. (Currently amended) The method according to claim 4, ~~further characterized in that~~ wherein the single-stranded regions are between 3 and 20 nucleotides long.

6. (Currently amended) The method according to claim 4, ~~further characterized in that~~ wherein the single-stranded regions are between 5 and 12 nucleotides long.

7. (Currently amended) The method according to claim 4, ~~further characterized in that~~ wherein the single-stranded region is 9 nucleotides long.

8. (Currently amended) The method according to claim ~~1~~ 4, ~~further characterized in that the~~ wherein the oligomers have a length of 20 to 150 nucleotides.

9. (Currently amended) The method according to claim ~~1~~ 4, ~~further characterized in that the~~ wherein the oligomers have a length of 35 to 60 nucleotides.

10. (Currently amended) The method according to claim 4, ~~further characterized in that~~ wherein the oligomers are present in a concentration of 1 pM to 1000 nM.

11. (Currently amended) The method according to claim 4, ~~further characterized in that~~ wherein the oligomers are present in a concentration of 1 nM to 100 nM.

12. (Currently amended) The method according to claim 1, further ~~characterized in that~~ comprising amplifying the DNA to be investigated ~~is amplified~~ after the enzyme treatment.

13. (Currently amended) The method according to claim 12, ~~further characterized in that~~ wherein the ~~amplification is conducted by means of~~ amplifying step comprises conducting a polymerase reaction.

14. (Currently amended) The method according to claim 13, ~~further characterized in that~~ wherein the ~~amplification is conducted by means of~~ amplifying step comprises conducting a polymerase chain reaction.

15. (Currently amended) The method according to claim 14, ~~further characterized in that~~ wherein the polymerase chain reaction ~~is conducted by means of~~ comprises using methylation-specific primers.

16. (Currently amended) The method according to claim 14, ~~further characterized in that~~ wherein the polymerase chain reaction comprises utilizing at least one methylation-specific blocker oligomer ~~is utilized in the polymerase chain reaction~~.

17. (Withdrawn) The method according to claim 12, further characterized in that a repeated enzymatic conversion with a cytidine deaminase is conducted after the amplification.

18. (Withdrawn) The method according to claim 12, further characterized in that the amplificates are analyzed by means of methods of length measurement, mass spectrometry or sequencing.

19. (Withdrawn) The method according to claim 12, further characterized in that the amplificates are analyzed by means of the primer extension method.

20. (Withdrawn) The method according to claim 12, further characterized in that the amplificates are analyzed by hybridization to oligomer arrays.

21. (Currently amended) The method according to claim 12, further ~~characterized in that~~ comprising analyzing the amplificates ~~are analyzed~~ with the use of real-time variants.

22. (Currently amended) The method according to claim 21, ~~further characterized in that~~ wherein the analyzing step comprises conducting a Taqman or a Lightcycler method ~~is conducted~~.

23. (Withdrawn) The method according to claim 12, further characterized in that several fragments are simultaneously amplified by means of a multiplex reaction.

24. (Withdrawn) Use of a method according to claim 1 for the diagnosis of cancer diseases or other disorders associated with a change in the methylation status.

25. (Withdrawn) Use of a method according to claim 1 for predicting undesired drug interactions, for the differentiation of cell types and tissues or for the investigation of cell differentiation.

26. (Withdrawn) Use of cytidine deaminases, which convert cytidine and 5-methylcytidine at different rates, for methylation analysis.

27. (Withdrawn) Use of cytidine deaminases, which convert cytidine and 5-methylcytidine at different rates, for the diagnosis of cancer diseases or other disorders associated with a change in the methylation status.

28. (Withdrawn) Use of cytidine deaminases, which convert cytidine and 5-methylcytidine at different rates, for predicting undesired drug interactions, for the differentiation of cell types and tissues or for the investigation of cell differentiation.

29. (Withdrawn) Use according to claim 24, further characterized in that the cytidine deaminase involves activation-induced cytidine deaminase (AID), a biologically active fragment of AID or a modification thereof.

30. (Withdrawn) A kit, which comprises the AID enzyme, a biologically active fragment of AID or a modification thereof as well as oligomers and the buffers necessary for the deamination, as well as optionally also a polymerase, primers and probes for an amplification and detection.